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RAW SEQUENCE LISTING   DATE: 04/08/2002
PATENT APPLICATION: US/09/782,587B   TIME: 16:03:58

Input Set : A:\0213us310-SEQUENCE_LISTING-Nov2001.txt
Output Set: N:\CRF3\04082002\I782587B.raw

     3 <110> APPLICANT: PEDERSEN, ANDERS H.   **ENTERED**
     4   ANDERSON, KIM V.
     5   BORNAES, CLAUS
     7 <120> TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
     9 <130> FILE REFERENCE: 31-001100US
    11 <140> CURRENT APPLICATION NUMBER: 09/782,587B
    12 <141> CURRENT FILING DATE: 2002-03-26
    14 <150> PRIOR APPLICATION NUMBER: PA 2000 00218
    15 <151> PRIOR FILING DATE: 2000-02-11
    17 <150> PRIOR APPLICATION NUMBER: 60/184,036
    18 <151> PRIOR FILING DATE: 2000-02-22
    20 <150> PRIOR APPLICATION NUMBER: 60/241,916
    21 <151> PRIOR FILING DATE: 2000-10-18
    23 <160> NUMBER OF SEQ ID NOS: 19
    25 <170> SOFTWARE: PatentIn Ver. 2.1
    27 <210> SEQ ID NO: 1
    28 <211> LENGTH: 406
    29 <212> TYPE: PRT
    30 <213> ORGANISM: Homo sapiens
    32 <220> FEATURE:
    33 <221> NAME/KEY: MOD_RES
    34 <222> LOCATION: (6)..(7)
    35 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
    37 <220> FEATURE:
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    39 <222> LOCATION: (14)
    40 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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    43 <221> NAME/KEY: MOD_RES
    44 <222> LOCATION: (16)
    45 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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    48 <221> NAME/KEY: MOD_RES
    49 <222> LOCATION: (19)..(20)
    50 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
    52 <220> FEATURE:
    53 <221> NAME/KEY: MOD_RES
    54 <222> LOCATION: (25)..(26)
    55 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
    57 <220> FEATURE:
    58 <221> NAME/KEY: MOD_RES
    59 <222> LOCATION: (29)
    60 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid

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 62 <220> FEATURE:
 63 <221> NAME/KEY: MOD_RES
 64 <222> LOCATION: (35)
 65 <223> OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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     69   1           5               10              15
W--> 71 Cys Lys Xaa Xaa Gln Cys Ser Phe Xaa Xaa Ala Arg Xaa Ile Phe Lys
     72         20              25              30
W--> 74 Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
     75         35              40              45
     77 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
     78         50              55              60
     80 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
     81   65              70              75              80
     83 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
     84             85              90              95
     86 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
     87             100             105             110
     89 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
     90             115             120             125
     92 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
     93         130             135             140
     95 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
     96 145             150             155             160
     98 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
     99             165             170             175
    101 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
    102             180             185             190
    104 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
    105             195             200             205
    107 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
    108     210             215             220
    110 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
    111 225             230             235             240
    113 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
    114             245             250             255
    116 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
    117             260             265             270
    119 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
    120             275             280             285
    122 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
    123     290             295             300
    125 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
    126 305             310             315             320
    128 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
    129             325             330             335
    131 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
    132             340             345             350
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134 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
135         355                 360                 365
137 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
138     370                 375                 ·380
140 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
141 385                 390                 395                 · 400
143 Leu Arg Ala Pro Phe Pro
144                 405
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 1338
149 <212> TYPE: DNA
150 <213> ORGANISM: Homo sapiens
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153 <221> NAME/KEY: CDS
154 <222> LOCATION: (115)..(1332)
156 <400> SEQUENCE: 2
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159 gccgtcttcg tcacccagga ggaagcccat ggcgtcctgc atcgccggcg ccgg gcc    117
160                                                             Ala
161                                                             1
163 aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc    165
164 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
165             5                 10                  15
167 aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac    213
168 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
169         20                  25                  30
171 gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag    261
172 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
173     35                  40                  45
175 tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg    309
176 Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
177 50                  55                  60                  65
179 cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc    357
180 Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
181                 70                  75                  80
183 gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc    405
184 Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly
185                 85                  90                  95
187 tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc    453
188 Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg
189         100                 105                 110
191 tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc    501
192 Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
193     115                 120                 125
195 acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac    549
196 Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn
197 130                 135                 140                 145
199 gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag    597
200 Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys
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201              150              155              160
203 ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg   645
204 Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu
205              165              170              175
207 tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac   693
208 Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His
209              180              185              190
211 tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc   741
212 Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly
213       195              200              205
215 gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg   789
216 Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val
217 210              215              220              225
219 gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac   837
220 Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His
221              230              235              240
223 gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac   885
224 Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His
225              245              250              255
227 gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg   933
228 Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu
229              260              265              270
231 gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac   981
232 Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp
233       275              280              285
235 cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg   1029
236 Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu
237 290              295              300              305
239 atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc   1077
240 Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro
241              310              315              320
243 aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag   1125
244 Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys
245              325              330              335
247 gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc   1173
248 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
249              340              345              350
251 ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc   1221
252 Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala
253       355              360              365
255 acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag   1269
256 Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu
257 370              375              380              385
259 tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg   1317
260 Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu
261              390              395              400
263 cgg gcc cct ttc cct tgataa                                          1338
264 Arg Ala Pro Phe Pro
265              405
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Input Set : A:\0213us310-SEQUENCE_LISTING-Nov2001.txt
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268 <210> SEQ ID NO: 3
269 <211> LENGTH: 406
270 <212> TYPE: PRT
271 <213> ORGANISM: Homo sapiens
273 <400> SEQUENCE: 3
274 Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu
275  1               5                  10                  15
277 Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys
278              20                  25                  30
280 Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
281          35                  40                  45
283 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
284      50                  55                  60
286 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
287  65                  70                  75                  80
289 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
290                  85                  90                  95
292 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
293              100                 105                 110
295 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
296          115                 120                 125
298 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
299      130                 135                 140
301 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
302 145                 150                 155                 160
304 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
305              165                 170                 175
307 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
308              180                 185                 190
310 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
311          195                 200                 205
313 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
314      210                 215                 220
316 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
317 225                 230                 235                 240
319 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
320              245                 250                 255
322 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
323              260                 265                 270
325 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
326          275                 280                 285
328 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
329      290                 295                 300
331 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
332 305                 310                 ·315                320
334 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
335              325                 330                 335
337 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
338          340                 345                 350
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VERIFICATION SUMMARY
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Input Set : **A:\0213us310-SEQUENCE_LISTING-Nov2001.txt**
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
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4/8/02